



Figure S1. Figure of the wild-type prawn (up) and the orange-red variant prawn (down).

Unigene0036561	-----MLPFLIAACALFSTTALGHIDVGVCVDIVDKYDFDPVPYLGRWYEQRFHIVY
Unigene0044620	MFEYLYLLSAALTVSHGMIISGEPKVDVGQCPNITNKYDfeaapylgvwyelerfpmsf
Unigene0028810	-----MNLNQMTSGQVFFRGPCPDIPPLKDFQPKRFLGRWYEIERFFVSY .. . * **: * **: . : ** *** : ** : :
Unigene0036561	E--IGQDCVNTIYDDLGDGYIGVHNMRASGNLTDISG--KAHLIAPG--VLSVEFLGY
Unigene0044620	E--AGQDCVTATYSVLDDVYIKVYNRARLLKGPIVDITG--RAHVIAPG--VLLVEFFTM
Unigene0028810	EDLAGSCWVENVLFEEKGRGHFTRLWDWKDHLSGRILSIENGITFGKKEPGLRYVVQRPSI * * . * . : : . * : . * . ** *:
Unigene0036561	PAG--DYHVLGTDYENFSCVYDCEQD--GPLRTQHAWLLTRAKIPDEATFEIANEVFARN
Unigene0044620	ENSGAEYHVLTDYEKFACVYNCVQT--GPVRAQYAWLLSRTTMDDETYNHAMGVFTDN
Unigene0028810	PILQGEYQILATDYYSYALAWQCMDFPLSLGHTEILWFLSKEQFPSYETEQTAKRLAAKF *: : * *** . : : . : * . : : * : * . * : * : :
Unigene0036561	GIDVSLFHRTHQGDDCPYVV
Unigene0044620	GIDISLFQTTYQASDCPYLE
Unigene0028810	GLHVKSLSQKQDR-THCPL-- * : . : : . : . **

Figure S2. Alignment of Apolipoprotein D amino acid sequences. Unigene0036561 and Unigene0044620, which were all with lower expression level in the orange-red variant, shared 65.63% sequence identity. Unigene0028810 which was with lower expression level in the orange-red variant, shared only 40.61% and 37.31% sequence identity with Unigene0036561 and Unigene0044620, respectively.